



Nucleotide

Protein

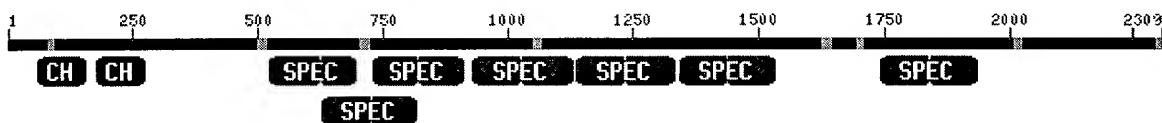
Translations

formatting **BLAST**Retrieve results for an
RID

WARNING: 6 illegal characters were removed: 6 Os

Your request has been successfully submitted and put into the Blast Queue.

Query = (2309 letters)

Putative conserved domains have been detected, click on the image below for detailed results.The request ID is **1085768146-22635-169323450554.BLASTQ3****Format!** or **Reset all**

The results are estimated to be ready in 23 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show Graphical Overview Linkout Sequence Retrieval NCBI-gi Alignment in **HTML**Use new formatter Masking Character **Default(X for protein, n for nucleotide)** Masking Color **Black**Number of: **Descriptions** **Alignments** **Alignment view** **Format for PSI-BLAST** with inclusion threshold: **0.005****Limit results by entrez query** or select from: **All organisms**



results of BLAST

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1085768146-22635-169323450554.BLASTQ3

Query=

(2309 letters)

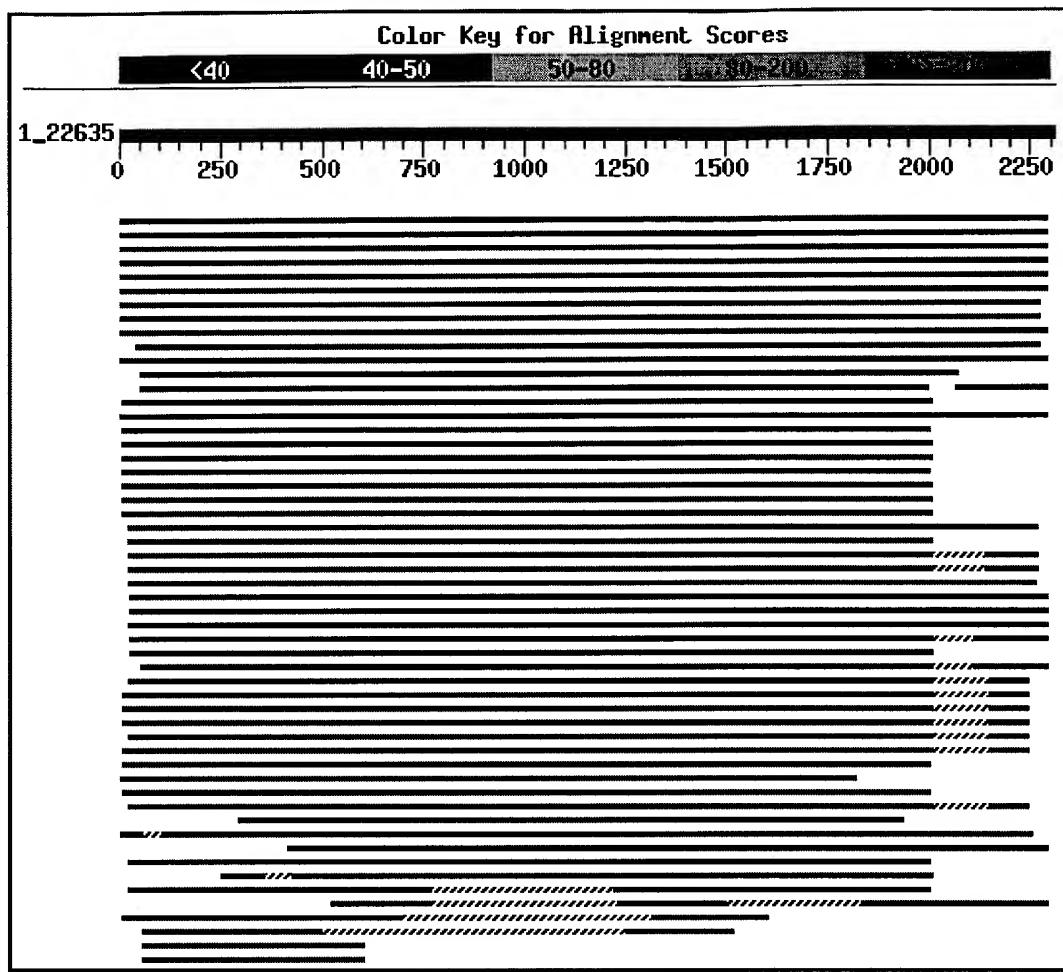
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,843,811 sequences; 610,536,048 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 253 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:	Score (bits)	E Value
gi 47227240 emb CAG00602.1 unnamed protein product [Tetrao...	2284	0.0
gi 38084794 ref XP_129130.3 spectrin beta 3 [Mus musculus]	3411	0.0
gi 31201699 ref XP_309797.1 ENSANGP00000023406 [Anopheles ...	1576	0.0
gi 47209542 emb CAF96656.1 unnamed protein product [Tetrao...	1895	0.0
gi 39594389 emb CAE71967.1 Hypothetical protein CBG19038 [...	1446	0.0
gi 25154697 ref NP_504749.2 beta-G spectrin, UNCoordinated...	1407	0.0
gi 7505762 pir T29140 hypothetical protein K11C4.3 - Caeno...	1395	0.0
gi 423777 pir A46147 spectrin beta chain - fruit fly (Dros...	1521	0.0
gi 47221201 emb CAG13137.1 unnamed protein product [Tetrao...	1660	0.0
gi 33340563 gb AAQ14859.1 beta spectrin IV [Homo sapiens]	1207	0.0
gi 17647191 ref NP_523388.1 CG5870-PA [Drosophila melanoga...	1519	0.0
gi 11066461 gb AAG28596.1 spectrin-like protein GTRAP41 [R...	3498	0.0
gi 29179635 gb AAH48851.1 Similar to beta-spectrin 3 [Mus ...	1112	0.0
gi 134798 sp P11277 SPCB_HUMAN Spectrin beta chain, erythro...	1660	0.0
gi 30348966 ref NP_787030.1 spectrin beta 2 isoform 1; bet...	2134	0.0
gi 17368942 sp Q9H254 SPCQ_HUMAN Spectrin beta chain, brain...	1316	0.0
gi 30315658 ref NP_842565.1 spectrin, beta, non-erythrocyt...	2009	0.0
gi 18859423 ref NP_571600.1 spectrin, beta, erythrocytic; ...	1818	0.0

gi 30794220 ref NP_115999.1	spectrin beta 4; beta-spectrin...	1317	0.0	L
gi 40353204 ref NP_066022.1	spectrin, beta, non-erythrocyt...	1308	0.0	L
gi 13435161 ref NP_079489.1	spectrin, beta, non-erythrocyt...	1313	0.0	L
gi 47210379 emb CAF95574.1	unnamed protein product [Tetrao...	1133	0.0	
gi 33303722 gb AAQ02380.1	non-erythroid spectrin beta [Rat...	2152	0.0	
gi 476928 pir A47213	beta-fodrin - human (fragment) >gi 42...	1177	0.0	L
gi 17367415 sp Q9QWN8 SPCP_RAT	Spectrin beta chain, brain 2...	3472	0.0	L
gi 11992162 gb AAG42473.1	spectrin beta IV [Homo sapiens]	1316	0.0	L
gi 5734146 gb AAD49858.1	beta-G spectrin [Caenorhabditis e...	1455	0.0	L
gi 47058982 ref NP_997687.1	erythroid spectrin beta [Rattu...	1645	0.0	L
gi 2506246 sp P15508 SPCB_MOUSE	Spectrin beta chain, erythr...	1634	0.0	L
gi 34855389 ref XP_218364.2	similar to betaIV-spectrin sig...	1197	0.0	L
gi 17562506 ref NP_504748.1	beta-G spectrin, UNCoordinated...	1409	0.0	L
gi 11602890 gb AAF93173.1	betaIV spectrin isoform sigma4 [...]	1302	0.0	L
gi 16117405 gb AAK38731.1	beta4-spectrin [Mus musculus] >g...	1313	0.0	L
gi 448251 prf 1916380A	beta spectrin (beta fodrin)	2085	0.0	
gi 7106421 ref NP_033286.1	spectrin beta 2 isoform 2; beta...	2008	0.0	L
gi 34866100 ref XP_234322.2	similar to Spectrin beta chain...	1653	0.0	L
gi 17976528 gb AAK77612.2	Uncoordinated protein 70, isofor...	1454	0.0	
gi 28277312 gb AAH46267.1	LOC398511 protein [Xenopus laevis]	1223	0.0	L
gi 34879632 ref XP_240072.2	similar to Spectrin beta chain...	2131	0.0	L
gi 9507135 ref NP_062040.1	beta-spectrin 3 [Rattus norvegi...	3471	0.0	L
gi 5902122 ref NP_008877.1	spectrin, beta, non-erythrocyti...	3308	0.0	L
gi 27413156 ref NP_000338.2	spectrin, beta, erythrocytic (...)	1664	0.0	L
gi 4507195 ref NP_003119.1	spectrin, beta, non-erythrocyti...	2182	0.0	L
gi 338440 gb AAA60578.1	spectrin Rouen (beta-220-218) muta...	1667	0.0	L
gi 15213122 gb AAK85734.1	beta-G spectrin [Brugia malayi]	1490	0.0	
gi 31201697 ref XP_309796.1	ENSANGP00000012507 [Anopheles ...]	1523	0.0	
gi 40216167 gb AAR82828.1	AT24411p [Drosophila melanogaster]	1071	0.0	
gi 47221024 emb CAG12718.1	unnamed protein product [Tetrao...	911	0.0	
gi 11602887 gb AAF93171.1	betaIV spectrin isoform sigma2 [...]	859	0.0	L
gi 10047361 dbj BAB13468.1	KIAA1642 protein [Homo sapiens]	843	0.0	L
gi 226515 prf 1516310A	beta spectrin	766	0.0	
gi 338330 gb AAA63259.1	muscle beta spectrin	748	0.0	
gi 2511779 gb AAC79502.1	beta III spectrin [Homo sapiens]	665	0.0	L
gi 31209523 ref XP_313728.1	ENSANGP00000017034 [Anopheles ...]	524	e-146	
gi 45552921 ref NP_995987.1	CG12008-PC [Drosophila melanog...	506	e-141	
gi 45552923 ref NP_995988.1	CG12008-PB [Drosophila melanog...	506	e-141	
gi 18481635 gb AAL73492.1	beta I spectrin form betaI sigma...	505	e-141	
gi 24656802 ref NP_523900.1	CG12008-PA [Drosophila melanog...	505	e-141	L
gi 7706190 ref NP_057726.1	spectrin, beta, non-erythrocyti...	500	e-139	L
gi 7655 emb CAA37939.1	betaH spectrin [Drosophila melanoga...	496	e-138	L
gi 420115 pir S29854	spectrin beta chain - dog (fragment) ...	496	e-138	L
gi 103502 pir A37792	spectrin beta-H chain - fruit fly (Dr...	488	e-136	
gi 444793 prf 1908227A	beta spectrin	488	e-135	
gi 11602888 gb AAF93172.1	betaIV spectrin isoform sigma3 [...]	481	e-134	L
gi 7506776 pir T23630	hypothetical protein R31.1 - Caenorh...	464	e-128	
gi 25155104 ref NP_741632.1	SMAll body size SMA-1, betaH c...	462	e-128	L
gi 39592126 emb CAE75346.1	Hypothetical protein CBG23326 [...]	455	e-126	

gi 18147604 dbj BAB83244.1 	beta IV-spectrin sigma6-A [Mus m...]	447	e-123	
gi 34856723 ref XP_238278.2 	similar to Spectrin beta chain...	412	e-113	
gi 2511781 gb AAC79503.1 	beta III spectrin [Homo sapiens]	348	1e-93	
gi 11992164 gb AAG42474.1 	spectrin beta IV [Homo sapiens]	337	2e-90	
gi 41054603 ref NP_955880.1 	actinin alpha 4; wu:fb53f05 [D...	336	5e-90	
gi 24639240 ref NP_726784.1 	CG4376-PB [Drosophila melanoga...	333	4e-89	
gi 24639238 ref NP_477484.2 	CG4376-PA [Drosophila melanoga...	332	6e-89	
gi 8186 emb CAA36042.1 	unnamed protein product [Drosophila...	332	9e-89	
gi 13123941 sp Q9QXQ0 AAC4_RAT	Alpha-actinin 4 (Non-muscle ...)	331	1e-88	
gi 11230802 ref NP_068695.1 	actinin alpha 4 [Mus musculus]...	331	1e-88	
gi 45384104 ref NP_990457.1 	alpha-actinin [Gallus gallus] ...	330	2e-88	
gi 1070611 pir FAFFAA	alpha-actinin - fruit fly (Drosophil...	330	2e-88	
gi 45387533 ref NP_991107.1 	Unknown (protein for MGC:77243...	330	2e-88	
gi 47212235 emb CAF96202.1 	unnamed protein product [Tetrao...	330	3e-88	
gi 25992501 gb AAN77132.1 	alpha-actinin [Danio rerio] >gi ...	330	3e-88	
gi 38197444 gb AAH61788.1 	Actn4 protein [Rattus norvegicus]	329	4e-88	
gi 12025678 ref NP_004915.2 	actinin, alpha 4 [Homo sapiens...	329	4e-88	
gi 2804273 dbj BAA24447.1 	alpha actinin 4 [Homo sapiens]	328	7e-88	
gi 31242387 ref XP_321624.1 	ENSANGP00000011796 [Anopheles ...]	328	8e-88	
gi 32766313 gb AAH54911.1 	Zgc:63559 protein [Danio rerio]	326	5e-87	
gi 37362178 gb AAQ91217.1 	actinin, alpha 2 [Danio rerio]	325	1e-86	
gi 17137758 ref NP_477485.1 	CG4376-PC [Drosophila melanoga...	324	1e-86	
gi 625303 pir FAHUAA	alpha-actinin 1 - human >gi 28334 emb...	324	1e-86	
gi 4501891 ref NP_001093.1 	actinin, alpha 1 [Homo sapiens]...	324	2e-86	
gi 30585329 gb AAP36937.1 	Homo sapiens actinin, alpha 1 [s...	324	2e-86	
gi 38018016 gb AAR08137.1 	brain-specific alpha actinin 1 i...	323	3e-86	
gi 13928936 ref NP_113863.1 	alpha actinin 4; alpha actinin...	323	4e-86	
gi 13591902 ref NP_112267.1 	actinin, alpha 1; non-muscle a...	322	5e-86	
gi 2345081 gb AAC02791.1 	beta-spectrin [Homo sapiens]	322	6e-86	
gi 539494 pir A42162	alpha-actinin 1 - chicken >gi 211083 ...	322	7e-86	
gi 13124665 sp P05094 AAC1_CHICK	Alpha-actinin 1 (Alpha-act...	322	7e-86	
gi 46395721 sp Q7TPR4 AAC1_MOUSE	Alpha-actinin 1 (Alpha-act...	322	9e-86	
gi 4557241 ref NP_001095.1 	skeletal muscle specific actini...	321	1e-85	

Alignments

>[gi|47227240|emb|CAG00602.1|](#) unnamed protein product [Tetraodon nigroviridis]
Length = 2413

Score = 2284 bits (5918), Expect = 0.0
Identities = 1439/2429 (59%), Positives = 1695/2429 (69%), Gaps = 170/2429 (6%)

Query: 3 STLSPTDFDSLEIQQYSDINNRWDL-P-DSWDNDSSARLFERSRI----- 48
ST+SPTDFDSLEIQ QY+DINNRWDL ++DWDN++SSARLFERSRI

Sbjct: 1 STISPTDFDSLEIQQQYNDINNRWDLAAETDWDNENSSARLFERSRIKALAAMDWDHRNR 60

Query: 49 -----MLADEREAVQKKTFTKVVNSHLARVTCRVGDLYSXX 84

L DEREAVQKKTFTKVVNSHL RVTCR+GDLY+
 Sbjct: 61 EPSLSPAAFVNQVQYANILEGRFKQLQDEREAVQKKTFTKVVNSHLGRVTCRIGDLYTDL 120
 Query: 85 XXXXXXXXXXXXEVLSGETLPKPTKGRMRIHCLEND--LQFLKEQKVHLENMGSHDIVDGN 142
 EVLSGE LP+PTKGRMRIHCLEND LQFLKEQKVHLENMGSHDIVDGN
 Sbjct: 121 RDGRMLIRLLEVLSGEQLPRPTKGRMRIHCLENDVKALQFLKEQKVHLENMGSHDIVDGN 180
 Query: 143 HRLTLGLVWTIILRFQIQDISVETEDNKEKKSAKDALLWCQMKTAGYPNVNVHNFTSW 202
 HRLTLGL+WTIILRFQIQDISVETEDNKEKKSAKDALLWCQMKTAGYPNVN+HNFTSW
 Sbjct: 181 HRLTLGLIWTIILRFQIQDISVETEDNKEKKSAKDALLWCQMKTAGYPNVNIHNFTSW 240
 Query: 203 RDGLAFNAIVHKHRPDLLFESLKKCNAHYNLQNAFNLAEKELGLTKLLDPEDVNVDQPD 262
 RDGLAFNAIVHKHRPD+DFE+LK+ NAHYNLQNAFN+AEKELGLTKLLDPEDVNVDQPD
 Sbjct: 241 RDGLAFNAIVHKHRPDLLFENLKRNSAHYNLQNAFNVAEKELGLTKLLDPEDVNVDQPD 300
 Query: 263 EKSIITYVATYYHYFSKM-MLAVEGKRIGKVLDHAMEAEHLVEKYESLASELLQWIEQTI 321
 EKSIITYVA YYHYFSKM LAVEGKRIGKVLD+A+EA+ L+EKYE+LASELLQWIEQTI
 Sbjct: 301 EKSIITYVAPYYHYFSKMKALAVEGKRIGKVLDYIAEADQLIEKYETLASELLQWIEQTI 360
 Query: 322 GTFNDRQLANSLSGVQNQLQSFNSYRTVEKPPKFTEKGNLEVLLFTIQSKL-MNNQKVYT 380
 T NDRQLANSLS VQNQLQ+FNSYRTVEKPPKFTEKGNLEVLLFTIQSK+ NNQKVY
 Sbjct: 361 VTLNDRQLANSLSAVQNQLQAFNSYRTVEKPPKFTEKGNLEVLLFTIQSKMRANNQKVYM 420
 Query: 381 PREGRLLISDIN-MWERLE-MEHERELALRTELIRQEKEQL-MRFDR--WMRETWLSENO 435
 P+EG+LISDIN WERLE EHERELALR ELIRQEKE L RFDR MRETWLSENO
 Sbjct: 421 PKEGKLISDINKAWERLEKAEHERELALRNELIRQEKEMLAARFDRKAAMRETWLSENO 480
 Query: 436 RLVSQDNFGLEL--MVERMVKHEAIETDIVAYSGRVQAVDAVMELMEH--YHDIKRM-R 490
 RLVSQDNFG L + RKHEAIETDI AY RV AV AV +E YHD++RI+ R
 Sbjct: 481 RLVSQDNFGTNLGAVEAATRKHEAIETDIGAYWERVERAAVQAVARELEAEGYHDVRRILAR 540
 Query: 491 QNNVARLWDF-XXXXXXXXXXXXXXXXXQVFQDLYLMDWMAEMKGRLQSQDLGKHLAG 549
 ++NV RLW++ Q++FQ++ Y+MDWM +MKGRLQS D GKHL
 Sbjct: 541 RDNVRLWEYLKELLAARRERLNAHRDLQRLFQEMRYIMDWMGDMKGRLQSPDSGKHLHD 600
 Query: 550 VEDLLQLHELVEADIAVQAERV-MVSASALRFCDPGKEYRPCGPQLVSVRATLEQSYEA 608
 V DLLQ H LVEAD + QAER+ V +A RF + Y+PC P LVSE+V L Q+YE
 Sbjct: 601 VLDLLQKHTLVEADSSAQAEARIKAVQGAAQRFTSYEQAYKPCPGLVSEKVDLLGQAYEE 660
 Query: 609 LCELMTRMR--LEESRRLWRFLEVGEEAEAWVREQQHLLASAETGRDLTGVLRLNKHTA 666
 L +L + R LE+SRRWL+FLW+VGE AW+REQ+ +LAS + GRDLT L LL+KH A
 Sbjct: 661 LGQLAVKRREQLEDSRRLWQFLWDVGEEAAWIREQEQLASGDCGRDLTSALHLLSKHEA 720
 Query: 667 LRGEMSGRLGPLKLTLEQGQQQLVAEGHPGANQASTXXXXXXXXXXXXXXXXXXM-- 724
 R EM+ R GPL ++ G+ L+ EGH GA + +
 Sbjct: 721 FRDEMAARYGPLSNSIAVGEALIKEGHFGAPEVRERIEDIRGQWSHLEETSQLREQSLKE 780
 Query: 725 --SLYQFQADANDMEAWLVDALRLVSSPEVGHDEFSTQALAR-QHMLEEEIM-HRPTLDA 780
 +L+QFQ DANDMEAW+++ R VSS EVGHDEFSTQ LAR Q +EEEI HRP +D+
 Sbjct: 781 SVALHQFQTDANDMEAWIMETFRQVSSQEVGHDEFSTQTLARKQREIEEEIKSHRPLIDS 840
 Query: 781 LRE--QWLPPALSHTPEVQGRVPTLEQHYEELQAMG---EMMLEMLAFYMLSEAGACG 834
 L E Q LP A + PEV GR+P +EQ YEEL+++ + + LA Y M SEAGAC
 Sbjct: 841 LHEQAQALPQAYVNFPEVDGRLPAIEQRYEELESLSVARRQALEGALALYRMFSEAGACL 900
 Query: 835 LWVEEKEQWLNGLALPERLEDPEVVQQRFETLEPEEMNAL-MRITAVSDIAEQLLSPPG-- 891
 +WVEEKEQ L+G+ +P +LED EVVQQRFETLEPEEMN L R+T V+ AEQLLS
 Sbjct: 901 VWVEEKEQRLHGMEIPTKLEDLEVQQRFETLEPEEMNNL GARVTVNQKAEQLLSSDSCN 960
 Query: 892 KDRIIGTQEQLNQRWQQFRSLAGGK--GLTSALSIQNYHLECTETQAWMREKTKVIESTQ 949

KD+I T++QLN RW++F LAG K L SAL+I QNYHLEC E Q WM+EKTIVIESTQ
 Sbjct: 961 KDQIHQTRDQLNDRWKEFEQLAGQKKQDLESALNIQNYHLECNEIQTWMKEKTIVIESTQ 1020

Query: 950 DLGNLALQRLAGTERDLEAISARVGELETQEANALM-GHPAQAPAINTRLGEVQT 1008
 LGNLAGV+ALQRKL G ERDLEAI ++ +L EA L HP QA I RL E+Q
 Sbjct: 1021 GLGNLALQVMAIQRKLTGMERDLEAIQGKLDLRNEAEKLAREHPDQAGEIQGRLTEIQE 1080

Query: 1009 GWEDLM-TMRRREESLGEARRLQDFLRSLDDFQAWLGRTQAVASXXXXXXXXXXXX 1067
 WEDL TM+RREESLGEA +LQ FLR LDDFQ WL RTQAVAS
 Sbjct: 1081 VWEDLNDTMKRREESLGEASKLQGFLRDLDDFQTLWSRTQAVASEDIPSLPEAESLLA 1140

Query: 1068 QH-MLRGEVE-MQSEYSRLRTLGEEVTRDQADPQCLFLRQRLEALGTGWEELGRMWESRQ 1125
 QH ++ EV+ + Y ++R +GEEVT+ Q D Q +FL QRL+AL TGW EL RMWE+R
 Sbjct: 1141 QHESIKNEVDNYKEDYEKMRRAVGEVTQGQTDAQHMFIAQRLQALDTGWHELRRMENRH 1200

Query: 1126 GRLAQAHGFQGFLRDAHQEGVLSSQEYVLSHTEMPGTLQ--MDMIKKLEDFMSTMDANG 1183
 LAQA FQ FLRDA+QAE L+SQEYVLSHTEMP +LQ + IKK EDF++T +A+
 Sbjct: 1201 SLLAQAFDFQTFLRDAKQAEFLNSQEYVLSHTEMPQLQGAAEAIKKHEDFLTTTEASE 1260

Query: 1184 ERIRGLLEAGRQLVSKGNIHAEKIQE-MDSIEKRHRKNQEAVQQLGRLRDNRQQHFLQ 1242
 E+I ++E+GR+L++ N +++KIQE +DSI +RHRKN+EA +LL +L+DNRE QHFLQ
 Sbjct: 1261 EKINSVVESGRRLINDCNANSKIQEKVDSILERHRKNKEAANELLAALKDNRELQHFLQ 1320

Query: 1243 DCQELKLWIDEKMLTAQDVSYDEARNLHTWKWQKHQAFMAELM-NKDWLKDVKDKEGRELTL 1301
 D QEL LWI+EKMLTAQD+SYDEARNLH+KWQKHQAFMAEL NKDWLKD+DKEG+ L
 Sbjct: 1321 DGQELTLWINEKMLTAQDMSYDEARNLHSWKWQKHQAFMAELASNKDWLKDIDKEGQALVA 1380

Query: 1302 EKPELKVLVSEKLEDLHRRWDELETTTQA-MRSLF DAN-MELFAQSCSALESWLESLQAQ 1359
 EKPELK +V + L+DL R+W+ELE TTQ + LFDAN ELF QSCSAL+ WL++L+ Q
 Sbjct: 1381 EKPELKPVVEQTLQDLQRQWEELEGGTTQTKAQCLFDANRAELFTQSCSALDVWLKNLEGQ 1440

Query: 1360 LHSDDYKDLTSVNILLKKQQMLEREMAVREKEVEAIQQAQALA--QEDQSAGEVE-RTSM 1416
 L SDDYKDLTSVNILLKK QMLE +M VREKEV++Q+QALA QED EV+ +
 Sbjct: 1441 LQSDDYKDLTSVNILLKKHQMLEHQMEVREKEVQSLQSQALALSQEDAGLTEVDGQQRR 1500

Query: 1417 VEEKFM-LCQPMKDRCCRRLQASREQHQFHRDVEDEILWVTERLPMASSLEHGKDLPSVQL 1475
 V + F L +P+ R +RL AS+E HQF+RD+EDEILWV ER+P+A+S +HGKDL P+VQL
 Sbjct: 1501 VTDNFSNLQEPNLRRQRLLASKEAHQFNRDLEDEILWVKERMPATSTDHGKDLPTVQL 1560

Query: 1476 LMKKNOTLQKEIQGHEPRIADLKERQRTLRTWGPE-----LAELQEMWKRLSHEEL 1527
 L+KKNQTLQKEIQGH+PRI D+ R +T E L ELQ++W L E +
 Sbjct: 1561 LIKKNQTLQKEIQGHQPRIDDIHRRSKTQSVDGERQSVQEERLCELQDLWSHLIAETDK 1620

Query: 1528 RGKRLEEA-LMQQFYRD-MEAEAWMGEQELHMMGQE--KDELSAQAEVKKHQVLEQALAD 1583
 R RL EA QQFY D EAEAWMGEQELHM+ +E KDE SA +KKHQ LEQAL D
 Sbjct: 1621 RHTRLIEANRAQQFYADAAEAEAWMGEQELHMLSEEKAKDEQSALVMLKKHQSLQALED 1680

Query: 1584 YAQTIKQLM-SSQDMIDHEHPESTRLTIRQAQVDKL YAGLKELAGXXXXXXXXXXXX 1642
 YAQTI QL SS+ M++ E+PES R+T+RQAQVDKL YAGLK+LA
 Sbjct: 1681 YAQTIHQLANSRSLMVNSENPESERITLRQAQVDKL YAGLKDLAEERRGQLQESLRLTQL 1740

Query: 1643 XXXXDDLEQWIQEREVVM-SHELGQDYEHVTMLRDKFREFSRDTSTIGQERVDSXXXXXX 1701
 DDLEQWI EREVV SHELGQDYEHVTMLRDKFREF+RDTSTIGQERV
 Sbjct: 1741 KREVDDLEQWIAEREVVAGSHELGQDYEHVTMLRDKFREFARDTSTIGQERVGVNALAD 1800

Query: 1702 XXXXXXHMW-ATVAEKDSLNEAWADLLELLDTRGQVLW--YELQRFLHGARQALARVQH 1758
 H+ ++AEWKD LNEAWADLLEL+DTR Q+L YEL RF A + L R++
 Sbjct: 1801 DLIESGHIENISTIAEWKDGLNEAWADLLELIDTRQMLAASYELHRFHQDAMEVLGRIKE 1860

Query: 1759 KQQQLPDGTGRDLN-MEALQRRHCAYEHDQALSTQVQQVQDDGLRLQ-MYAGD-MEEIG 1815

K++ LP GRDLN ++ L R+H +E+DIQALS QV QVQDD RLQ YAG+ ++I
 Sbjct: 1861 KREGLPSDLGRDLNKVQHLHRQHNTFENDIQALSGQVNQVQDDAARLQKAYAGEKADDIH 1920

Query: 1816 RHMQAVAEAW-AQLQGSSMRRQLLLDTDKFRFF-MVRELMILWMDGINLQMDAQERPRDV 1873
 R AV AW L+ RR LL+DT +KFRFF MVR+LMLWMDG+NLQ+DA + PRDV
 Sbjct: 1921 RSEHAVISAWEGGLEAGQARRVLLVDTVEKFRFFNMVRDMLWMDGVNLQIDAHDSPRDV 1980

Query: 1874 SSADLVIKNQQGIM-EIEA-MDRFSACIDMGQELLARNHYM-EEISEKLSQLQSRRQETA 1930
 SSA LVI N Q I EIE D F+ACI+MG LL NYH +EI EKL QLQ +R++
 Sbjct: 1981 SSAGLVIANHQDIKSEIETRADSFTACIEMGNTLLNNHYASDEIREKLQKQLEKREKID 2040

Query: 1931 EKWQEKMWDWLQLVLEVLFGRDAGM-EAWLCSQEPLVRSAAELGCTVDEV-SLIKRHEAFQ 1988
 +KQW+KMD LQ+VLEVL FGRDA + E+WL QEPLVR+AELG VDEV SLIKRHEAF+
 Sbjct: 2041 KKWQDKMDHLQIVLEVLFGRDAYIAESWLAGQEPLVRAAELGANVDEVESLIKRHEAFE 2100

Query: 1989 KSAVAVWEERFSALEKLITALXXXXXXXXXXXXXXXXXXPTEPMASQPEGSLVDGQRVL 2048
 K A WE+RF LEKLT L P A S +
 Sbjct: 2101 KLAAGWEDRFVLLKEKLTTLEEQEMQRREEERARRPPTPPAEEAVDMTESHIHDS--- 2157

Query: 2049 DTAWDGTQSKL-PPS-----TQAPSINGVCTDTESSQ-----PLLEQQRLEQSN 2091
 A Q++L PPS + P I + S L + + +S
 Sbjct: 2158 -AARPCEQARLFPPSKFHDFSHLPVIGCSSARSHPSSYRVFSRSPPFTLFLRPQGSESE 2216

Query: 2092 XPEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRSSES A HVATLPARGAELSAQE QME 2151
 GPG +G SS R A + +P +ES E ME
 Sbjct: 2217 SVNGPGRDSGLASS-----RLEASATLPNRGGAES-----EPEAME 2252

Query: 2152 GTLCRKQEMEAFNK---NRSWQNVYCVLRRGSLGFYKDAWSA--GVPYHGEVPVSLAMQ- 2205
 G LCRKQEME+ +K RSWQNVYCVLR+GSLGFYKD SA G+PYHGEVP+SLA
 Sbjct: 2253 GMLCRKQEMESHSKKAATRSWQNVYCVLRKGSLGFYKDGSASNGIPYHGEVPISLAEAV 2312

Query: 2206 GSVAFDYRKHKVFKLGLQDGKEYLFQAKDEAEMSSWRVVMIA TASSASGE-PEEPVV 2264
 VA DY+KRKHVFKL L DGKEYLFQAKDEAEM SW+R +++ + S SG+ P P V
 Sbjct: 2313 CEVAHDYKKRKHKVFKLRLGDGKEYLFQAKDEAEMGSWIR--SILGSVPSGSGDSPGGPRV 2370

Query: 2265 PSASRGLTMMTMPPVSQPEGGSIVLRSKD 2293
 SR +TM + P S G + +R+KDG
 Sbjct: 2371 --LSRAMT MPPISPSSAEGGGVTMRNKDG 2397

>gi|38084794|ref|XP_129130.3|  spectrin beta 3 [Mus musculus]
 Length = 2409

Score = 3411 bits (8844), Expect = 0.0
 Identities = 2074/2393 (86%), Positives = 2090/2393 (87%), Gaps = 100/2393 (4%)

Query: 1 MSSTLSPTDFDSLEIQGQYS DINNRWDL PDSDWDNDSSSARLFERSRI----- 48
 MSSTLSPTDFDSLEIQGQYS DINNRWDL PDSDWDNDSSSARLFERSRI
 Sbjct: 1 MSSTLSPTDFDSLEIQGQYS DINNRWDL PDSDWDNDSSSARLFERSRIKALAAFINPAQ 60

Query: 49 -----MLADEREAVQKKFTKVN SHLARVTCRVGDLYSXXXXXXXXXXEVLS 98
 L DEREAVQKKFTKVN SHLARVTCRVGDLYS EVLS
 Sbjct: 61 YASVLEGRFKQLQDEREAVQKKFTKVN SHLARVTCRVGDLYSDLRDGRNLLRLLEVLS 120

Query: 99 GETLPKPTKGRMRIHCLEND--LQFLKEQKVHLENMGSHDIVDGNHRLTLGLVWTIILR 156
 GETLPKPTKGRMRIHCLEND LQFLKEQKVHLENMGSHDIVDGNHRLTLGLVWTIILR
 Sbjct: 121 GETLPKPTKGRMRIHCLENDVKALQFLKEQKVHLENMGSHDIVDGNHRLTLGLVWTIILR 180

Query: 157 FQIQDISVETEDNKEKSAKDALLWCQMKTAGYPNVNVHNFTTSWRDGLAFNAIVHKHR 216

Sbjct: 181 FQIQDISVETEDNKEKSAKDALLWCQMKTAGYPNVNVHNFTTSWRDGLAFNAIVHKHR
 FQIQDISVETEDNKEKSAKDALLWCQMKTAGYPNVNVHNFTTSWRDGLAFNAIVHKHR 240

 Query: 217 PDLLDFESLKKCNAHYNLQNAFNLAEKELGLTKLLDPEDVNVDQPDEKSIITYVATYYHY 276
 PDLLDFESLKKCNAHYNLQNAFNLAEKELGLTKLLDPEDVNVDQPDEKSIITYVATYYHY

 Sbjct: 241 PDLLDFESLKKCNAHYNLQNAFNLAEKELGLTKLLDPEDVNVDQPDEKSIITYVATYYHY 300

 Query: 277 FSKM-MLAVEGKRIGKVLDHAMEAEHLVEKYESLASELLQWIEQTIGTFNDRQLANSLSG 335
 FSKM LAVEGKRIGKVLDHAMEAEHLVEKYESLASELLQWIEQTIT NDRQLANSLSG

 Sbjct: 301 FSKMKALAVEGKRIGKVLDHAMEAEHLVEKYESLASELLQWIEQTIVTLNDRQLANSLSG 360

 Query: 336 VQNQLQSFNSYRTVEKPPKFTKGNLEVLLFTIQSKL-MNNQKVYTPREGRЛИSDIN-MW 393
 VQNQLQSFNSYRTVEKPPKFTKGNLEVLLFTIQSKL NNQKVYTPREGRЛИSDIN W

 Sbjct: 361 VQNQLQSFNSYRTVEKPPKFTKGNLEVLLFTIQSKL RANQKVYTPREGRЛИSDINKAW 420

 Query: 394 ERLE-MEHERELALRTELIRQEKEQL-MRFDR--WMRETWLSENQRLVSQDNFGLELMV 449
 ERLE EHRELALRTELIRQEKEQL RFDR MRETWLSENQRLVSQDNFGLEL

 Sbjct: 421 ERLEKAEHERELALRTELIRQEKEQLAARFDRKAAMRETWLSENQRLVSQDNFGLELAA 480

 Query: 450 --EMVRKHEAIETDIVAYSGRVQAVDAV рел--EHYHDIKRI-MRQNNVARLWDF-XXX 503
 VRKHEAIETDIVAYSGRVQAVDAV + EHYHDIKRI RQNNVARLWDF

 Sbjct: 481 VEA AVRKHEAIETDIVAYSGRVQAVDAAAELAAEHYHDIKRIAARQNNVARLWDFLRQM 540

 Query: 504 XXXXXXXXXXXXXXXQKVFDLLYLMDWMAEMKGRLQSQDLGKHLAGVEDLLQLHELVEAD 563
 QKVFDLLYLMDWMAEMKGRLQSQDLGKHLAGVEDLLQLHELVEAD

 Sbjct: 541 VAARRERLLNLELQKVFDLLYLMDWMAEMKGRLQSQDLGKHLAGVEDLLQLHELVEAD 600

 Query: 564 IAVQAERV-MVSASALRFCDPGKEYRPCGPQLV релSERVATLEQSYEALCELMT--RMRLEE 620
 IAVQAERV VSASALRFCDPGKEYRPC PQLV релSERVATLEQSYEALCEL R RLEE

 Sbjct: 601 IAVQAERVR A VASALRFCDPGKEYRPCDPQLV релSERVATLEQSYEALCELAA TRRARLEE 660

 Query: 621 SRR LWRFLWEVGEAEAWVREQQHLLASAETGRDLTGVRLLNKHTALRGEMSGRLGPLKL 680
 SRR LWRFLWEVGEAEAWVREQQHLLASA+TGRDLTGVRLLNKHTALRGEMSGRLGPLKL

 Sbjct: 661 SRR LWRFLWEVGEAEAWVREQQHLLASA DTGRDLTGVRLLNKHAALRGEMSGRLGPLKL 720

 Query: 681 TLEQGQLVAEGHPGANQASTXXXXXXXXXXXXXXXXX---SLYQFQADANDM 736
 TLEQGQLVAEGHPGANQAST + SLYQFQADANDM

 Sbjct: 721 TLEQGQLVAEGHPGANQASTRAAELQAQWERLEALAEERAQQLAQAAASLYQFQADANDM 780

 Query: 737 EAWLVDALRLVSSPEVGHDEFSTQALARQH-MLEEEI-MHRPTLDALREQ--WLPPALSH 792
 EAWLVDALRLVSSPEVGHDEFSTQALARQH LEEEI HRPTLDALREQ LPPALSH

 Sbjct: 781 EAWLVDALRLVSSPEVGHDEFSTQALARQH RALEEEI RHRPTLDALREQAAALPPALSH 840

 Query: 793 TPEVQGRVPTLEQHYEELQAMG---EMMLEMLAFYTMLEAGACGLWVEEKEQWLNGLA 848
 TPEVQGRVPTLEQHYEELQA + LAFYTMLEAGACGLWVEEKEQWLNGLA

 Sbjct: 841 TPEVQGRVPTLEQHYEELQARAGERARALEAALAFYTMLEAGACGLWVEEKEQWLNGLA 900

 Query: 849 LPERLEDPEVVQQRFETLEPEMNAL-MRITAVSDIAEQLL--SPPGKDRIIGTQEQLNQR 905
 LPERLED EVVQQRFETLEPEMNAL R+TAV+DIAEQLL SPPGKDRIIGTQEQLNQR

 Sbjct: 901 LPERLEDLEVQQRFETLEPEMNAL AARVTAVNDIAEQLL KASPPGKDRIIGTQEQLNQR 960

 Query: 906 WQQFRSLAGGK--GLTSALSIQNYHLECTETQAWMREKTKVIESTQDLGNDLAGVLALQR 963
 WQQFRSLA GK LTSALSIQNYHLECTETQAWMREKTKVIESTQ LGNDLAGVLALQR

 Sbjct: 961 WQQFRSLADGKKAALTSALSIQNYHLECTETQAWMREKTKVIESTQGLGNDLAGVLALQR 1020

 Query: 964 KLAGTERDLEAISARVGELTQEANAL-MGHPAQAPAINTRLGEVQTGWEDL-TMRRREE 1021
 KLAGTERDLEAISARVGELTQEANAL GHHPAQAPAINTRLGEVQ GWEDL TMRRREE

 Sbjct: 1021 KLAGTERDLEAISARVGELTQEANAL AAGHPAQAPAINTRLGEVQAGWEDL RATMRRREE 1080

 Query: 1022 SLGEARRLQDFLRSLDDFQAWLGRTQAVASXXXXXXXXXXXXQH-MLRGEVE-MQS 1079

SLGEARRLQDFLRLSLDDFQAWLGRTQTAVAS QH LRGEVE QS
 Sbjct: 1081 SLGEARRLQDFLRLSLDDFQAWLGRTQTAVASEEGPATLPEAEALLAQHAALRGEVERAQS 1140

Query: 1080 EYSRLRTLGEEVTRDQADPQCLFLRQRLEALGTGWEELGRMWESRQGRLAQAHGFQGFLR 1139
 EYSRLRTLGEEVTRDQADPQCLFLRQRLEALGTGWEELGRMWESRQGRLAQAHGFQGFLR
 Sbjct: 1141 EYSRLRTLGEEVTRDQADPQCLFLRQRLEALGTGWEELGRMWESRQGRLAQAHGFQGFLR 1200

Query: 1140 DARQAEGVLSSQEYVLSHTEMPGTLQM--DMIKKLEDFMSTMDANGERIRGLLEAGRQLV 1197
 DARQAEGVLSSQEYVLSHTEMPGTLQ IKKLEDFMSTMDANGERIRGLLEAGRQLV
 Sbjct: 1201 DARQAEGVLSSQEYVLSHTEMPGTLQAADAIKKLEDFMSTMDANGERIRGLLEAGRQLV 1260

Query: 1198 SKGNIHAEKIQE-MDSIEKRHRKNQEAVQQLLGRRLRDNREQQHFLQDCQELKLWIDEKML 1256
 SKGNIHAEKIQE DSIKRHRKNQEAVQQLLGRRLRDNREQQHFLQDCQEL+LWIDEKML
 Sbjct: 1261 SKGNIHAEKIQEADSIKRHRKNQEAVQQLLGRRLRDNREQQHFLQDCQELRLWIDEKML 1320

Query: 1257 TAQDVSYDEARNLHTWKWQKHQAFMAEL-MNKDWLDKVDKEGRELTLEKPELKVLVSEKLE 1315
 TAQDVSYDEARNLHTWKWQKHQAFMAEL NKDWLDKVDKEGRELTLEKPELK+VSEKLE
 Sbjct: 1321 TAQDVSYDEARNLHTWKWQKHQAFMAELAANKDWLDKVDKEGRELTLEKPELKVVVSEKLE 1380

Query: 1316 DLHRRWDELETTTQA-MRSLF DAN-MELFAQSCSALESWLESLOAQLHSDDYKDLTSVN 1373
 DLHRRWDELETTTQA RSLFDAN ELFAQSCSALESWLESLOAQLHSDDYKDLTSVN
 Sbjct: 1381 DLHRRWDELETTTQA KARSLFDANRAELFAQSCSALESWLESLOAQLHSDDYKDLTSVN 1440

Query: 1374 ILLKKQQMLEREMAVREKEVE--AIQAQALAQEDQSAGEVERTS-MVEEKF-MLCQPMKD 1429
 ILLKKQQMLEREMAVREKEVE QAQALAQEDQSAGEVERTS VEEKF LCQPMK+
 Sbjct: 1441 ILLKKQQMLEREMAVREKEVEAIQAQALAQEDQSAGEVERTSRAVEEKFRALCQPMKE 1500

Query: 1430 RCRRLQASREQHQFHRDVEDEI LWVTERLPMASSLEHGKDLPSVQLMKNQTLQKEI QG 1489
 RCRRL ASREQHQFHRDVEDEI LWVTERLPMASSLEHGKDLPSVQLMKNQTLQKEI QG
 Sbjct: 1501 RCRRLHASREQHQFHRDVEDEI LWVTERLPMASSLEHGKDLPSVQLMKNQTLQKEI QG 1560

Query: 1490 HEPRIADLKERQRTLRT--WGPELAELOEMWKRLSHELELRGKRLEEAL-MQQFYRD-ME 1545
 HEPRIADLKERQRTL T GPELAELOEMWKRLSHELELRGKRLEEAL QQFYRD E
 Sbjct: 1561 HEPRIADLKERQRTLGTAAAGPELAELOEMWKRLSHELELRGKRLEEALRAQQFYRDAAE 1620

Query: 1546 AEAWMGEQELHMMGQE--KDELSAQAEVKHKHQVLEQALADYAQTIKQL-MSSQDMIDHEH 1602
 AEAWMGEQELHMMGQE KDELSAQAEVKHKHQVLEQALADYAQTIKQL SSQDMIDHEH
 Sbjct: 1621 AEAWMGEQELHMMGQEAKDELSAQAEVKHKHQVLEQALADYAQTIKQLASSQDMIDHEH 1680

Query: 1603 PESTRLTIROAQVDKLYAGLKELAGXXXXXXXXXXXXXXDDLEQWIQEREVV-MS 1661
 PESTRLTIROAQVDKLYA LKELAG DDLEQWIQEREVV S
 Sbjct: 1681 PESTRLTIROAQVDKLYASLKELAGERRLQEHRLCQLRRELDDLEQWIQEREVVAA 1740

Query: 1662 HELGQDYEHVTMLRDKFREFS DTSTIGQERVDSXXXXXXXXXXHMW-ATVAEWKDSL 1720
 HELGQDYEHVTMLRDKFREFS+DTSTIGQERVDS H ATVAEWKDSL
 Sbjct: 1741 HELGQDYEHVTMLRDKFREFSKDTSTIGQERVDSANALANGLIAGGHAARATVAEWKDSL 1800

Query: 1721 NEAWADLLELLDTRGQL--WYELQRFLH GARQALARVQHKQQQLPDGTGRDLN-MEALQ 1777
 NEAWADLLELLDTRGQL YELQRFLH GARQALARVQHKQQQLPDGTGRDLN EALQ
 Sbjct: 1801 NEAWADLLELLDTRGQLAAAYELQRFLH GARQALARVQHKQQQLPDGTGRDLNAAEALQ 1860

Query: 1778 RRHCAYEHDIQALSTQVQQVQDDGLRLQ-MYAGD-MEEIGRHMQAVA EWAQ LQGSS-MR 1834
 RRHCAYEHDIQALSTQVQQVQDDG RLQ YAGD EEIGRHMQAVA EWAQ LQGSS R
 Sbjct: 1861 RRHCAYEHDIQALSTQVQQVQDDGQRLQKAYAGDKAEEIGRHMQAVA EWAQ LQGSSAAR 1920

Query: 1835 QL LDTTDKFRFF-MVREMLWMDGINLQMDAQERPRDVSSADLVIKNQQGI-MEIEA- 1891
 QL LDTTDKFRFF VREMLWMDGINLQMDAQERPRDVSSADLVIKNQQGI EIEA
 Sbjct: 1921 QL LDTTDKFRFFKAVREMLWMDGINLQMDAQERPRDVSSADLVIKNQQGI KAEIEAR 1980

Query: 1892 MDRFSACIDMGQELLARNHY-MEEISEKLSQLQSRRQETAEKWQEKM DWLQLVLEVLFVFG 1950

DRFS+CIDMGQELLAR+HY EEISEKLSQLQSRRQETA+KWQEKMDSLQLVLEVLVFG
 Sbjct: 1981 ADRFSSCIDMGQELLARSHYAAEIESEKLSQLQSRRQETADKWQEKMDSLQLVLEVLVFG 2040

Query: 1951 RDAGM-EAWLCSQEPLVRSALGCTVDEV-SLIKRHEAFQKSAVAAWEERFSALEKLTALEX 2008
 RDAGM EAWLCSQEPLVRSALGCTVDEV SLIKRHEAFQKSAVAAWEERFSALEKLTALEX
 Sbjct: 2041 RDAGMAEWLCSQEPLVRSALGCTVDEVESLIKRHEAFQKSAVAAWEERFSALEKLTALEX 2100

Query: 2009 XXXXXXXXXXXXXXXXXXXXPPTEPMASQPEGSLVDGQRVLDTAWDGTQSKLPPSTQAPSI 2068
 PPTSEPMASQPEGSLVDGQRV DTAWDGTQSKLPPSTQAPSI+
 Sbjct: 2101 ERENERKRKREEEERRKQPPTSEPMASQPEGSLVDGQRVPDTAWDGTQSKLPPSTQAPSV 2160

Query: 2069 NGVCTDTESSQPLLEQQRLEQSNXPEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRS 2128
 NGVCTDT+SSQPLLEQQRLEQSN PEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRS
 Sbjct: 2161 NGVCTDTSQPLLEQQRLEQSNVPEGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRS 2220

Query: 2129 SESAHVATLPARGAELSAQEIQMEGLCRKQEMEAFNK---NRSWQNVYCVLRRGSLGFYK 2185
 SE+AH ATLP RG ELSAQEQMEG LCRKQEMEAFNK NRSWQNVYCVLRRGSLGFYK
 Sbjct: 2221 SEAAGATLPTRGPELSAQEQMEGMLCRKQEMEAFNKKAANRSWQNVYCVLRRGSLGFYK 2280

Query: 2186 D--AWSAGVPYHGEVPVSLA-MQGSVAFDYRKRKHVKLGLQDGKEYLFQAKDEAEMSSW 2242
 D A SAGVPYHGEVPVSLA QGSVAFDYRKRKHVKLGLQDGKEYLFQAKDEAEMSSW
 Sbjct: 2281 DARAASAGVPYHGEVPVSLARAQGSVAFDYRKRKHVKLGLQDGKEYLFQAKDEAEMSSW 2340

Query: 2243 LRVVN-MIATASSASGEPEEPVVPASRGLT-MMTMPPVSQPEGSIVLRSKDG 2293
 LRVVN IATASSA GE EEPVVPASRGLT MTMPPVSQPEGSIVLRSKDG
 Sbjct: 2341 LRVVNAAIATASSAPGESEEPVVPASRGLTRAMTMPPVSQPEGSIVLRSKDG 2393

>gi|31201699|ref|XP_309797.1| ENSANGP00000023406 [Anopheles gambiae]
gi|30178366|gb|EAA45309.1| ENSANGP00000023406 [Anopheles gambiae str. PEST]
 Length = 2362

Score = 1576 bits (4081), Expect = 0.0
 Identities = 1052/2351 (44%), Positives = 1437/2351 (61%), Gaps = 117/2351 (4%)

Query: 25 RWD-----LPDSDWDNDSSSARLFERSRI-MLADEREAVQKKTFTKWKVNNSHLARVT 74
 RWD + D ++D +SS+RLFERSRI LA+ERE+VQKKTFTKWKVNNSHL RV
 Sbjct: 9 RWDPGPGNEFIEDIEYDGGNSSRLFERSRIKALAEERESVQKKTFTKWKVNNSHLRVN 68

Query: 75 CRVGDLYSXXXXXXXXXXXXEVLSGETLPKPTKGRMRIHCLENVD--LQFLKEQKVHLEN 132
 + DLY EVLSGE LP+PTKG+MRIHCLENVD LQFL+EQ+VHLEN
 Sbjct: 69 SPIKDLYVDMRDGKNLKLLEVLSGERLPRPTKGKMRHIHCLENVDKALQFLREQRVHLEN 128

Query: 133 MGSHDIVDGNHRLTLGLVWTIILRFQIQDISVETEDNKEKSAKDALLWCQMKTAGYPN 192
 +GSHDIVDGN L LGL+WTIILRFQIQDI+E DNKE KSAKDALLWCQMKTAGY N
 Sbjct: 129 IGHSHDIVDGNASLNLGLIWTIILRFQIQDITIEETDNKETKSAKDALLWCQMKTAGYHN 188

Query: 193 VNVHNFTTSWRDGLAFNAIVHKHRPDLLDFESLKKCNAHYNLQNAFNLAELGLTKLLD 252
 VNV NFTTSWRDGLAFNAI+HKHRPD+ F+ L K N NL NAFN+AE++LGLTKLLD
 Sbjct: 189 VNVRNFTTSWRDGLAFNAIIHKHRPDLIQFDKLSKTNPIQNLNNAFNVAEEKLGLTKLLD 248

Query: 253 PEDVNVDQPDEKSIITYVATYYHYFSKM-MLAVEGKRIGKVLHDHMEAELVYESLAS 311
 ED+ VD PDEKSIITYV TYYHYFSK+ V+GKRIGKV+ AM+ + ++ +YESL S
 Sbjct: 249 AEDIFVDHPDEKSIITYVVTYYHYFSKLKQETVQGKRIGKVVGIAMDNDRMINEYESLTS 308

Query: 312 ELLQWIEQTIGTFNDRQLANSLSGVQNQLQSFNSYRTVEKPPKFTEGNLEVLLFTIQSK 371
 ELL+WIE TI DR NSL GVQ QL F++YRTVEKPPKF EKGNLEVLLFT+QSK
 Sbjct: 309 ELLKWIEVTIVQLGDRHFVNSLGVQQQLAQFSNYRTVEKPPKFVEKGNLEVLLFTLQSK 368